

SEQUENCE LISTING

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Crafton, Corey

Walsh, Holly

<120> Polynucleotides Encoding A Feedback Resistant Aspartokinase From Corynebacterium

<130> 040049

<140> 09/722,441

<141> 2000-11-28

<150> US 60/173,707

<151> 1999-12-30

<150> US 60/184,130

<151> 2000-02-22

<160> 37

<170> PatentIn version 3.0

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<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

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gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct
96
Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala

20 25 30

gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat
144
Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp

35 40 45

gaa ctt cta gaa ctt gca gcg gca gtg aat ccc gtt ccg cca gct cgt
192
Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg

50 55 60

gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc
240
Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu

65 70 75 80

gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act
288 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr

85 90 95

ggc tct cag gct ggt gtg ctc acc acc gag cgc cac gga aac gca cgc
336 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg

100 105 110

att gtt gac gtc aca ccg ggt cgt gtg cgt gaa gca ctc gat gag ggc
384 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly

115 120 125

aag atc tgc att gtt gct ggt ttt cag ggt gtt aat aaa gaa acc cgc
432 Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg

130 135 140

gat gtc acc acg ttg ggt cgt ggt tct gac acc act gca gtt gcg
480 Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala

145 150 155 160

ttg gca gct gct ttg aac gct gat gtg tgt gag att tac tcg gac gtt
528 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val

165 170 175

gac ggt gtg tat acc gct gac ccg cgc atc gtt cct aat gca cag aag
576 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys

180

185

190

ctg gaa aag ctc agc ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc
624
Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly

195

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tcc aag att ttg gtg ctg cgc agt gtt gaa tac gct cgt gca ttc aat
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Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn

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gtg cca ctt cgc gta cgc tcg tct tat agt aat gat ccc ggc act ttg
720
Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu

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att gcc ggc tct atg gag gat att cct gtg gaa gaa gca gtc ctt acc
768
Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr

245

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ggt gtc gca acc gac aag tcc gaa gcc aaa gta acc gtt ctg ggt att
816
Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile

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tcc gat aag cca ggc gag gct gcc aag gtt ttc cgt gcg ttg gct gat
864

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp

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285

gca gaa atc aac att gac atg gtt ctg cag aac gtc tcc tct gtg gaa
912
Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu

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gac ggc acc acc gac atc acg ttc acc tgc cct cgc gct gac gga cgc
960
Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg

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315

320

cgt gcg atg gag atc ttg aag aag ctt cag gtt cag ggc aac tgg acc
1008
Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr

325

330

335

aat gtg ctt tac gac gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct
1056
Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala

340

345

350

ggc atg aag tct cac cca ggt gtt acc gca gag ttc atg gaa gct ctg
1104
Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu

355

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365

cgc gat gtc aac gtg aac atc gaa ttg att tcc atc tct gag atc cgc
1152
Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg

370

375

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att tcc gtg ctg atc cgt gaa gat gat ctg gat gct gct gca cgt gca
1200
Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala

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395

400

ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat
1248
Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr

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gca ggc acc gga cgc taa
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<213> Corynebacterium glutamicum

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35 40 45

Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg

100

105

110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
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Ala Gly Thr Gly Arg
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<213> *Corynebacterium glutamicum*

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atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt
96
Met Arg Thr Phe Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg

20 25 30

ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc
144
Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly

35 40 45

acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc
192
Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu

50 55 60

aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag
240
Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys

65 70 75 80

cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac
288
Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn

85 90 95

tct tct gct tgg cgc aag gac gac gag gtt cca cta atc gtc tct gag

336

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu

100

105

110

gtg aac cct tcc gac aag gat tcc ctg gtc aag ggc att att gcg aat
384

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn

115

120

125

cct aac tgc acc acc atg gct gca atg cca gtg ctg aag cca ctg cac
432

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His

130

135

140

gat gcc gct ggt ctt gta aag ctt cac gtt tcc tct tac cag gct gtt
480

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val

145

150

155

160

tcc ggt tct ggt ctt gca ggt gtg gaa acc ttg gca aag cag gtt gct
528

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala

165

170

175

gca gtt ggc gac cac aac gtt gag ttc gtc cat gat gga cag gct gct
576

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala

180

185

190

gac gca ggc gat gtc gga cct tac gtt tcc cca atc gct tac aac gtg
624

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val

195

200

205

ctg cca ttc gcc gga aac ctc gtc gat gac ggc acc ttc gaa acc acc gac

672
Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

gaa gag cag aag ctg cgc aac gaa tcc cgc aag att ctc ggc ctc cca
720
Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

gac ctc aag gtc tca ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc
768
Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag
816
His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu
260 265 270

cag gcg cag gag atc ttg ggt gcc gct tca ggc gtc gag ctt gtc gac
864
Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp
275 280 285

gtc cca acc cca ctt gca gct gcc ggc att gac gaa tcc ctc gtt gga
912
Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

cgc atc cgt cag gac tcc act gtc gac gac aac cgc ggt ctg gtt ctc
960
Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305 310 315 320

gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc acc att
1008

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile

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Gln Ile Ala Glu Leu Leu Val Lys

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<210> 4

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<213> Corynebacterium glutamicum

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Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
50 55 60

Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
100 105 110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
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325 330 335

Gln Ile Ala Glu Leu Leu Val Lys
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gtt gga gta gca atg gtt act cca ttc acg gaa tcc gga gac atc gat
96
Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp

20

25

30

atc gct gct ggc cgc gaa gtc gcg gct tat ttg gtt gat aag ggc ttg
 144
 Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu

35

40

45

gat tct ttg gtt ctc gcg ggc acc act ggt gaa tcc cca acg aca acc
 192
 Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr

50

55

60

gcc gct gaa aaa cta gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg
 240
 Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly

65

70

75

80

gat cgg gcg aag ctc atc gcc ggt gtc gga acc aac aac acg cgg aca
 288
 Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr

85

90

95

tct gtg gaa ctt gcg gaa gct gct gct tct gct ggc gca gac ggc ctt
 336
 Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu

100

105

110

tta gtt gta act cct tat tac tcc aag ccg agc caa gag gga ttg ctg
 384
 Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu

115

120

125

gcg cac ttc ggt gca att gct gca gca aca gag gtt cca att tgt ctc
 432
 Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu

130

135

140

tat gac att cct ggt cgg tca ggt att cca att gaa tct gat acc atg
480
Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met

145

150

155

160

aga cgc ctg agt gaa tta cct acg att ttg gcg gtc aag gac gcc aag
528
Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys

165

170

175

ggc gac ctc gtt gca gcc acg tca ttg atc aaa gaa acg gga ctt gcc
576
Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala

180

185

190

tgg tat tca ggc gat gac cca cta aac ctt gtt tgg ctt gct ttg ggc
624
Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly

195

200

205

gga tca ggt ttc att tcc gta att gga cat gca gcc ccc aca gca tta
672
Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu

210

215

220

cgt gag ttg tac aca agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg
720
Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg

225

230

235

240

gaa atc aac gcc aaa cta tca ccg ctg gta gct gcc caa ggt cgc ttg
768
Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu

245

250

255

ggt gga gtc agc ttg gca aaa gct gct ctg cgt ctg cag ggc atc aac
816
Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn

260

265

270

gta gga gat cct cga ctt cca att atg gct cca aat gag cag gaa ctt
864
Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu

275

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<213> Corynebacterium glutamicum

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Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
260 265 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
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act att gtg gca gca gtc aat gag tcc gac gat ctg gag ctt gtt gca
96
Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala

20 25 30

gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac aac ggc gct
144

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala

35

40

45

gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg ggc aac ctg
192

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu

50

55

60

gag ttc tgc atc aac aac ggc att tct gcg gtt gga acc acg ggc
240

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly

65

70

75

80

ttc gat aat gct cgt ttg gag cag gtt cgc gcc tgg ctt gaa gga aaa
288

Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys

85

90

95

gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc tct gcg gtg
336

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val

100

105

110

ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc gaa tca gct
384

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala

115

120

125

gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca cct tca ggc
432

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly

130

135

140

acc gcg atc cac act gct cag ggc att gct gcg gca cgc aaa gaa gca
480
Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
145 150 155 160

ggc atg gac gca cag cca gat gcg acc gag cag gca ctt gag ggt tcc
528
Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
165 170 175

cgt ggc gca agc gta gat gga atc cca gtt cac gca gtc cgc atg tcc
576
Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
180 185 190

ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag ggt cag acc
624
Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
195 200 205

ttg acc atc aag cag gac tcc tat gat cgc aac tca ttt gca cca ggt
672
Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
210 215 220

gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc cta gtc gta
720
Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
225 230 235 240

gga ctt gag cat tac cta ggc ctg taa
747
Gly Leu Glu His Tyr Leu Gly Leu
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<210> 8

<211> 248

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<213> *Corynebacterium glutamicum*

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35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
65 70 75 80

Phe Asp Asn Ala Arg Leu Glu Gln Val Arg Ala Trp Leu Glu Gly Lys
85 90 95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
100 105 110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
115 120 125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
130 135 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
145 150 155 160

Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
165 170 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
180 185 190

Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
195 200 205

Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
210 215 220

Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
225 230 235 240

Gly Leu Glu His Tyr Leu Gly Leu
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<210> 9

<211> 1023

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<213> *Corynebacterium glutamicum*

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<222> (1)..(1023)

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48
Met His Phe Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

gat tac aag aac atg acc aac atc cgc gta gct atc gta ggc tac gga
96
Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

aac ctg gga cgc agc gtc gaa aag ctt att gcc aag cag ccc gac atg
144
Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

gac ctt gta gga atc ttc tcg cgc cgg gcc acc ctc gac aca aag acg
192
Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
50 55 60

cca gtc ttt gat gtc gcc gac gtg gac aag cac gcc gac gac gtg gac
240
Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

gtg ctg ttc ctg tgc atg ggc tcc gcc acc gac atc cct gag cag gca
288
Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

cca aag ttc gcg cag ttc gcc tgc acc gta gac acc tac gac aac cac
336
Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

cgc gac atc cca cgc cac cgc cag gtc atg aac gaa gcc gcc acc gca
384
Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

gcc ggc aac gtt gca ctg gtc tct acc ggc tgg gat cca gga atg ttc
432
Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

tcc atc aac cgc gtc tac gca gcg gca gtc tta gcc gag cac cag cag
480
Ser Ile Asn Arg Val Tyr Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

cac acc ttc tgg ggc cca ggt ttg tca cag ggc cac tcc gat gct ttg
528
His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
165 170 175

cga cgc atc cct ggc gtt caa aag gcc gtc cag tac acc ctc cca tcc
576
Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
180 185 190

gaa gaa gcc ctg gaa aag gcc cgc cgt ggc gaa gcc ggc gac ctc acc
624
Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
195 200 205

gga aag caa acc cac aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc
672
Gly Lys Gln Thr His Lys Arg Arg Gly Glu Ala Gly Asp Leu Ala
210 215 220

gac cac gag cgc atc gaa aac gac atc cgc acc atg cct gat tac ttc
720
Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225 230 235 240

gtt ggc tac gaa gtc gaa gtc aac ttc atc gac gaa gca acc ttg gac
768
Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp
245 250 255

gcc gag cac acc ggc atg cca cac ggc gga cac gtg atc acc acc ggc
816
Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
260 265 270

gac acc ggt ggc ttc aac cac acc gtg gaa tac atc ctg aag ctg gac
864
Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
275 280 285

cga aac cca gat ttc acc gct tct tca cag atc gct ttc ggc cgc gca
912
Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
290 295 300

gct cac cgc atg aag cag cag ggc caa agc ggt gct ttc acc gtc ctc
960
Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305 310 315 320

gaa gtt gct cca tac ttg ctc tcc ccg gag aac ttg gat gat ctg atc
1008
Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
325 330 335

gca cgc gac gtc taa
1023
Ala Arg Asp Val

340

<210> 10

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 10

Met His Phe Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
1 5 10 15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
20 25 30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
35 40 45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
50 55 60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65 70 75 80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
85 90 95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
100 105 110

Arg Asp Ile Pro Arg His Gln Val Met Asn Glu Ala Ala Thr Ala
115 120 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
130 135 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145 150 155 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
165 170 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
180 185 190

Glu Glu Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
195 200 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
210 215 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225 230 235 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Leu Asp
245 250 255

Ala Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
260 265 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
275 280 285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
290 295 300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305 310 315 320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
325 330 335

Ala Arg Asp Val
340

<210> 11

<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1338)

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48

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro

1 5 10 15

cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg
96

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val

20 25 30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc

144

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val

35

40

45

gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc
192

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe

50

55

60

ggt gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag
240

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys

65

70

75

80

acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg
288

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala

85

90

95

tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc
336

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser

100

105

110

cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg
384

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala

115

120

125

ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa
432

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu

130

135

140

ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac

480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

gtg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc
528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc
576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

ggt tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg
624
Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc
672
Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

gaa ggc ttc aag ctg gca gca gag cgc gtg ttg ggc ctg tac tca cag
720
Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

atc cac agc gaa cta ggt gtc gcc ctt cct gag ctg gac ctc ggt ggc
768
Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca

816

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala

260

265

270

gaa gtc gcc tcc gac cta ctc acc gca gtc gga aaa atg gca gcg gaa
864

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu

275

280

285

cta ggc atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc
912

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile

290

295

300

gca ggc ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa aac
960

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn

305

310

315

320

gtc cac gta gac gac gac aaa acc cgc cgc tac gta gcc gtc gac gga
1008

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly

325

330

335

ggc atg tcc gac aac atc cgc cca gca ctc tac ggc tcc gaa tac gac
1056

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp

340

345

350

gcc cgc gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc
1104

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg

355

360

365

atc gtg ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa

1152

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu

370

375

380

atc tac cca tct gac atc acc agc ggc gac ttc ctc gca ctc gca gcc
1200

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala

385

390

395

400

acc ggc gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca
1248

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr

405

410

415

cgg ccc gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg
1296

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu

420

425

430

cgc cgc gaa acc ctc gac gac atc ctc tca cta gag gca taa
1338

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala

435

440

445

<210> 12

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro

1 5 10 15

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20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu
275 280 285

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile
290 295 300

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asn
305 310 315 320

Val His Val Asp Asp Lys Thr Arg Arg Tyr Val Ala Val Asp Gly
325 330 335

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp
340 345 350

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg
355 360 365

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu
370 375 380

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala
385 390 395 400

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr
405 410 415

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu
420 425 430

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
435 440 445

<210> 13

<211> 1338

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1338)

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Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

cgc aat gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg
96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val

20 25 30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc
144

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc
192 Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

ggt gga cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag
240 Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca
288 Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

tcc atc aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc
336 Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg
384 Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

ttg gtt caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa
432 Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

cta gaa ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac
480

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

gtg ttg atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc
528 Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc
576 Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

ggt tcc gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg
624 Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

aac ctg gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc
672 Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

gaa ggc ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag
720 Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

atc cac agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc
768 Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

gga tac ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca

816

Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala

260

265

270

gaa gtt gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa
864

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu

275

280

285

cta ggc atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc
912

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile

290

295

300

gca ggc ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac
960

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp

305

310

315

320

gtc cac gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga
1008

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly

325

330

335

ggc atg tcc gac aac atc cgc cca gca ctc tac ggc tcc gaa tac gac
1056

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp

340

345

350

gcc cgc gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc
1104

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg

355

360

365

atc gtg ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa

1152

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu

370

375

380

atc tac cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc
1200

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala

385

390

395

400

acc ggc gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca
1248

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr

405

410

415

cgg ccc gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg
1296

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu

420

425

430

cgc cgc gaa acg ctc gac gac atc ctc tca cta gag gca taa
1338

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala

435

440

445

<210> 14

<211> 445

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro

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15

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20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu
275 280 285

Leu Gly Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile
290 295 300

Ala Gly Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp
305 310 315 320

Val His Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly
325 330 335

Gly Met Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp
340 345 350

Ala Arg Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg
355 360 365

Ile Val Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu
370 375 380

Ile Tyr Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala
385 390 395 400

Thr Gly Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr
405 410 415

Arg Pro Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu
420 425 430

Arg Arg Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
435 440 445

<210> 15

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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(753)

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48

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1

5

10

15

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg
96

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala

20

25

30

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat

144

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp

35

40

45

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc
192

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile

50

55

60

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg
240

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met

65

70

75

80

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac
288

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His

85

90

95

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga
336

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly

100

105

110

gaa tcg gaa gta gtg gtg ccc act ctc atc gat gaa gat ccg cag ttg
384

Glu Ser Glu Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu

115

120

125

cgt gaa ctt ttc atg cac gcc atg gat gag tct cgg ttc gct ttc aat
432

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn

130

135

140

gag ctg ctt aat gcg ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca

480
Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

ctt tta agg aaa aag cag gct cgt caa gca gct cgc gct gtg ctg ccc
528
Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165 170 175

aac gct aca gag tcc aga atc gtg gtg tct gga aac ttc cgc acc tgg
576
Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

agg cat ttc att ggc atg cga gcc agt gaa cat gca gac gtc gaa atc
624
Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

cgc gaa gta gcg gta gga tgt tta aga aag ctg cag gta gca gcg cca
672
Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

act gtt ttc ggt gat ttt gag att gaa act ttg gca gac gga tcg caa
720
Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

atg gca aca agc ccg tat gtc atg gac ttt taa
753
Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

<210> 16

<211> 250

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 16

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
115 120 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
130 135 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145 150 155 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
165 170 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
180 185 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
195 200 205

Arg Glu Val Ala Val Gly Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
210 215 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225 230 235 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
245 250

<210> 17

<211> 551

<212> DNA

<213> *Corynebacterium glutamicum*

<400> 17
aaccgggtgtg gagccgacca ttccgcgagg ctgcactgca acgaggtcgt agttttggta
60

catggcttct ggccagttca tggattggct gccgaagaag ctatagggcat cgccaccagg
120

gccaccggag ttaccgaaga tggtgccgtg ctttcgcct tgggcaggga ctttgacaaa
180

gcccacgctg atatcgccaa gtgaggggatc agaatagtgc atgggcacgt cgatgctgcc
240

acattgagcg gaggcaatat ctacctgagg tggcattct tcccagcgga tgtttcttg
300

cgctgctgca gtggcattg atacaaaaaa ggggctaagc gcagtcgagg cggcaagaac
360

tgctactacc ttttttattg tcgaacgggg cattacggct ccaaggacgt ttgtttctg
420

ggtcagttac cccaaaaagc atatacagag accaatgatt tttcattaaa aaggcaggga
480

tttgttataa gtatgggtcg tattctgtgc gacgggtgt a ctcggctag aatttctccc
540

catgacacca g
551

<210> 18

<211> 365

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(365)

<400> 18

gtg gcc gaa caa gtt aaa ttg agc gtg gag ttg ata gcg tgc agt tct
48

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser

1

5

10

15

ttt act cca ccc gct gat gtt gag tgg tca act gat gtt gag ggc gcg

96

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala

20

25

30

gaa gca ctc gtc gag ttt gcg ggt cgt gcc tgc tac gaa act ttt gat
144

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp

35

40

45

aag ccg aac cct cga act gct tcc aat gct gcg tat ctg cgc cac atc
192

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile

50

55

60

atg gaa gtg ggg cac act gct ttg ctt gag cat gcc aat gcc acg atg
240

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met

65

70

75

80

tat atc cga ggc att tct cgg tcc gcg acc cat gaa ttg gtc cga cac
288

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His

85

90

95

cgc cat ttt tcc ttc tct caa ctg tct cag cgt ttc gtg cac agc gga
336

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly

100

105

110

gaa tcg gaa gta gtg gtg ccc act ctc at

365

Glu Ser Glu Val Val Val Pro Thr Leu Ile

115

120

<210> 19

<211> 122

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 19

Met Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
1 5 10 15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
20 25 30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
35 40 45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
50 55 60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
65 70 75 80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
85 90 95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
100 105 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile
115 120

<210> 20

<211> 833

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(833)

<400> 20

atg gct aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca
48
Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro

1 5 10 15

cgc aat gca gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg
96
Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val

20 25 30

cct ctg cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc
144
Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val

35 40 45

gac gag gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc
192

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe

50 55 60

ggt gga cca ggc aat gtg cac tac gca tcc aaa gcg ttc ctg acc aag
240
Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys

65 70 75 80

acc att gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gcg
288
Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

tcc atc aat gaa ctg ggc att gcc ctg gcc gct ggt ttc ccg gcc agc
336
Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

cgt atc acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg
384
Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

ttg gtt caa aac ggt gtc ggg cat gtg gtg ctg gac tcc gcg cag gaa
432
Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

ttg gaa ctg ctg gat tac gtt gcc gct ggt gaa ggc aag atc cag gac
480
Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

ttg ttg atc cgc gtg aag cca ggt atc gaa gcc cac acc cac gag ttc
528
Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe
165 170 175

atc gcc act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc
576
Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

ggt tcc gca ttc gaa gca gcg aaa gca gcc aac aat gca gag aac ttg
624

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu

195

200

205

aac ctg gtt ggt ctg cac tgc cat gtt ggt tcc cag gtg ttc gac gcc
672

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala

210

215

220

gaa ggc ttc aag ctg gca gca gag cgc gtg ttg ggc ctg tac tca cag
720

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln

225

230

235

240

atc cac agc gaa cta ggt gtc gcc ctt cct gag ctg gac ctc ggt ggc
768

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly

245

250

255

gga tac ggc atc gcc tac act gca gat gag gaa cca ctc aac gtc gca
816

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala

260

265

270

gaa gtc gcc tcc gac ct
833

Glu Val Ala Ser Asp Leu

275

<210> 21

<211> 278

<212> PRT

<213> Corynebacterium glutamicum

<400> 21

Met Ala Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro
1 5 10 15

Arg Asn Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val
20 25 30

Pro Leu Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val
35 40 45

Asp Glu Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe
50 55 60

Gly Gly Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys
65 70 75 80

Thr Ile Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala
85 90 95

Ser Ile Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser
100 105 110

Arg Ile Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala
115 120 125

Leu Val Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu
130 135 140

Leu Glu Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp
145 150 155 160

Val Leu Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe

165

170

175

Ile Ala Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser
180 185 190

Gly Ser Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu
195 200 205

Asn Leu Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala
210 215 220

Glu Gly Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln
225 230 235 240

Ile His Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly
245 250 255

Gly Tyr Gly Ile Ala Tyr Thr Ala Asp Glu Glu Pro Leu Asn Val Ala
260 265 270

Glu Val Ala Ser Asp Leu
275

<210> 22

<211> 28

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 22
gggtacctcg cgaagtagca cctgtcac
28

<210> 23
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 23
gcggatcccc catcgccct caaaga
26

<210> 24
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 24
aacgggcggt gaagggcaac t
21

<210> 25
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 25
tgaaagacag gggtatccag a
21

<210> 26
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 26
ccatggtaacc aagtgcgtgg cgag
24

<210> 27
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 27
ccatggtaacc acactgtttc cttgc
25

<210> 28

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 28

ctggttccgg cgagtggagc cgaccattcc gcgagg

36

<210> 29

<211> 36

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 29

ctcgctccgg cgaggtcgga ggcaacttct gcgacg

36

<210> 30

<211> 6

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 30
ggtacc
6

<210> 31
<211> 18
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 31
ggatcttcac ctagatcc
18

<210> 32
<211> 16
<212> DNA
<213> Artificial

<220>
<223> Primer
<400> 32
ccctgataaaa tgcttc
16

<210> 33
<211> 25
<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 33

ccggagaaga tgtaacaatg gctac
25

<210> 34

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Primer

<400> 34

cctcgactgc agaccctag acacc
25

<210> 35

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 35

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr

405

410

415

Ala Gly Thr Gly Arg
420

<210> 36

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Asp Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 37

<211> 421

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 37

Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
1 5 10 15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
20 25 30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
35 40 45

Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg
50 55 60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
65 70 75 80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
85 90 95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
100 105 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
115 120 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
130 135 140

Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala
145 150 155 160

Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu

225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420